

Appl. No. 10/026,994
Amdt. dated April 4, 2005
Reply to Office action of November 5, 2004

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IN THE SPECIFICATION:

Please amend the paragraph at page 7, lines 5-7 as follows:

Figure 2 shows the complete protein (~~SEQ ID NO:5~~) encoded by the nucleotide sequence given in Figure 1. The predicted amino acid sequence (SEQ ID NO:2) and signal sequence (SEQ ID NO:3) based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1), wherein the signal sequence is indicated as bolded.

Please amend the paragraph at page 19, lines 3-6 as follows:

A Basic BLASTN search (go to world wide web www.ncbi.nlm.nih.gov/BLAST) of the non-redundant nucleic acid sequence database was conducted on September 12, 2001, with the *egl6* gene sequence presented in Figure 1 (SEQ ID NO:1), indicated no sequences producing significant alignments (i.e. with an E value of less than 10^{-5}).

Please amend the paragraph at page 24, lines 24-33 as follows:

A Basic BLASTP search (go to world wide web www.ncbi.nlm.nih.gov/BLAST) of the non-redundant protein database, conducted on September 12, 2001 with the EGVI amino acid sequence indicated 51% identity with GenBank Accession Number AB015511 (avicellase III of *Aspergillus aculeatus*), 49% sequence identity to GenBank Accession Number AJ292929 (CEL6 protein of *Agaricus bisporus*), 39% sequence identity to GenBank Accession Number AE007608 (probable secreted sialidase of *Clostridium acetabutylicum*), and 40% sequence identity to GenBank Accession Number AL031515 (probable secreted cellulase of *Streptomyces coelicolor*). These sequence similarities indicate that EGVI is a member of glycosyl hydrolase family 74 (Henrissat, B. and Bairoch, A. (1993) Biochem. J. 293:781-788).

Please amend the paragraph at page 29, lines 11-15 as follows:

Preferred culture conditions for a given filamentous fungus may be found in the scientific literature and/or from the source of the fungi such as the American Type Culture Collection (ATCC; go to world wide web <http://www.atcc.org/>). After fungal growth has been established, the cells are exposed to conditions effective to cause or

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permit the over expression of EGVI.

Please amend the paragraph at page 37, lines 29-33 as follows:

Exemplary computer programs which can be used to determine identity between two sequences include, but are not limited to, the suite of BLAST programs, e.g., BLASTN, BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly available on the Internet at world wide web ~~http://www.ncbi.nlm.nih.gov/BLAST/~~. See also, Altschul, *et al.*, 1990 and Altschul, *et al.*, 1997.